

PCT09

RAW SEQUENCE LISTING

DATE: 07/12/2001

PATENT APPLICATION: US/09/869,414

TIME: 07:53:08

Input Set : A:\6280Mseq.txt

Output Set: N:\CRF3\07122001\I869414.raw

4 <110> APPLICANT: Beinkowski et al.

6 <120> TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND

USES

8 THEREFOR

10 <130> FILE REFERENCE: 28341/6280M

C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/869,414

C--> 13 <141> CURRENT FILING DATE: 2001-06-27

15 <150> PRIOR APPLICATION NUMBER: 09/416,901

16 <151> PRIOR FILING DATE: 1999-10-13

18 <150> PRIOR APPLICATION NUMBER: 60/155,493

19 <151> PRIOR FILING DATE: 1999-09-23

21 <150> PRIOR APPLICATION NUMBER: 09/404,133

22 <151> PRIOR FILING DATE: 1999-09-23

24 <150> PRIOR APPLICATION NUMBER: PCT/US99/20881

25 <151> PRIOR FILING DATE: 1999-09-23

27 <150> PRIOR APPLICATION NUMBER: 60/101,594

28 <151> PRIOR FILING DATE: 1998-09-24

30 <160> NUMBER OF SEQ ID NOS: 73

32 <170> SOFTWARE: PatentIn Ver. 2.0

34 <210> SEQ ID NO: 1

35 <211> LENGTH: 1804

36 <212> TYPE: DNA

37 <213> ORGANISM: Homo sapiens

39 <400> SEQUENCE: 1

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 42 cgcgtagtgt cgcacacccc gggaccgggg acccctgccc agcgccacgc cgacggcttg 180
 43 gcgctcgccc tggagcctgc cctggcgctc ccgcggggcg ccgccaactt cttggccatg 240
 44 gtagacaacc tgcaggggga ctctggccgc ggctactacc tggagatgct gatcgggacc 300
 45 cccccgcaga agctacagat tctcgttgac actggaagca gtaactttgc cgtggcagga 360
 46 accccgcact cctacataga cactactttt gacacagaga ggtctagcac ataccgctcc 420
 47 aagggtcttg acgtcacagt gaagtacaca caaggaagct ggacgggctt cgttggggaa 480
 48 gacctcgtca ccatcccaaa aggtttcaat actttttttc ttgtcaacat tgccactatt 540
 49 tttgaatcag agaattttct tttgcctggg attaaatgga atggaatact tggcctagct 600
 50 tatgccacac ttgccaagcc atcaagttct ctggagacct tcttcgactc cctgggtgaca 660
 51 caagcaaaca tccccaacgt tttctccatg cagatgtgtg gagccggctt gcccgttgct 720
 52 ggatctggga ccaacggagg tagtcttgct ttgggtggaa ttgaaccaag tttgtataaa 780
 53 ggagacatct ggtatacccc tattaaggaa gagtgtgtact accagataga aattctgaaa 840
 54 ttggaaattg gaggccaaag ccttaatctg gactgcagag agtataacgc agacaaggcc 900
 55 atcgtggaca gtggcaccac gctgctgcgc ctgccccaga aggtgtttga tgcgggtggtg 960
 56 gaagctgttg cccgcgcac tctgattcca gaattctctg atggtttctg gactgggtcc 1020
 57 cagctggcgt gctggacgaa ttcggaacaa ccttgggtct acttccctaa aatctccatc 1080
 58 tacctgagag atgagaactc cagcaggtca ttccgtatca caatcctgcc tcagctttac 1140
 59 attcagccca tgatgggggc cggcctgaat tatgaatgtt accgattcgg catttcccca 1200
 60 tccacaaatg cgtggtgat cgggtgccacg gtgatggagg gcttctacgt catcttcgac 1260
 61 agagcccaga agagggtggg ctctgcagcg agccctgtg cagaaattgc aggtgtgca 1320
 62 gtgtctgaaa tttccgggccc tttctcaaca gaggatgtag ccagcaactg tgtccccgct 1380
 63 cagtctttga gcgagcccat tttgtggatt gtgtcctatg cgctcatgag cgtctgtgga 1440

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64 gccatcctcc ttgtcttaat cgtcctgctg ctgctgccgt tccgggtgtca gcgtcgcccc 1500
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66 gccaggcctg acctcaagca accatgaact cagctattaa gaaaatcaca ttccagggc 1620
67 agcagccggg atcgatggg gcgctttctc ctgtgccac cgtcttcaa tctctgttct 1680
68 gctcccagat gccttctaga ttactgtct tttgattctt gattttcaag ctttcaaata 1740
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73 <211> LENGTH: 518
74 <212> TYPE: PRT
75 <213> ORGANISM: Homo sapiens
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79 1 5 10 15
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82 20 25 30
84 Leu Arg Val Ala Ala Ala Thr Asn Arg Val Val Ala Pro Thr Pro Gly
85 35 40 45
87 Pro Gly Thr Pro Ala Glu Arg His Ala Asp Gly Leu Ala Leu Ala Leu
88 50 55 60
90 Glu Pro Ala Leu Ala Ser Pro Ala Gly Ala Ala Asn Phe Leu Ala Met
91 65 70 75 80
93 Val Asp Asn Leu Gln Gly Asp Ser Gly Arg Gly Tyr Tyr Leu Glu Met
94 85 90 95
96 Leu Ile Gly Thr Pro Pro Gln Lys Leu Gln Ile Leu Val Asp Thr Gly
97 100 105 110
99 Ser Ser Asn Phe Ala Val Ala Gly Thr Pro His Ser Tyr Ile Asp Thr
100 115 120 125
102 Tyr Phe Asp Thr Glu Arg Ser Ser Thr Tyr Arg Ser Lys Gly Phe Asp
103 130 135 140
105 Val Thr Val Lys Tyr Thr Gln Gly Ser Trp Thr Gly Phe Val Gly Glu
106 145 150 155 160
108 Asp Leu Val Thr Ile Pro Lys Gly Phe Asn Thr Ser Phe Leu Val Asn
109 165 170 175
112 Ile Ala Thr Ile Phe Glu Ser Glu Asn Phe Phe Leu Pro Gly Ile Lys
113 180 185 190
115 Trp Asn Gly Ile Leu Gly Leu Ala Tyr Ala Thr Leu Ala Lys Pro Ser
116 195 200 205
118 Ser Ser Leu Glu Thr Phe Phe Asp Ser Leu Val Thr Gln Ala Asn Ile
119 210 215 220
121 Pro Asn Val Phe Ser Met Gln Met Cys Gly Ala Gly Leu Pro Val Ala
122 225 230 235 240
124 Gly Ser Gly Thr Asn Gly Gly Ser Leu Val Leu Gly Gly Ile Glu Pro
125 245 250 255
128 Ser Leu Tyr Lys Gly Asp Ile Trp Tyr Thr Pro Ile Lys Glu Glu Trp
129 260 265 270
131 Tyr Tyr Gln Ile Glu Ile Leu Lys Leu Glu Ile Gly Gly Gln Ser Leu
132 275 280 285
134 Asn Leu Asp Cys Arg Glu Tyr Asn Ala Asp Lys Ala Ile Val Asp Ser

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135      290      295      300
137 Gly Thr Thr Leu Leu Arg Leu Pro Gln Lys Val Phe Asp Ala Val Val
138 305      310      315      320
140 Glu Ala Val Ala Arg Ala Ser Leu Ile Pro Glu Phe Ser Asp Gly Phe
141      325      330      335
143 Trp Thr Gly Ser Gln Leu Ala Cys Trp Thr Asn Ser Glu Thr Pro Trp
144      340      345      350
146 Ser Tyr Phe Pro Lys Ile Ser Ile Tyr Leu Arg Asp Glu Asn Ser Ser
147      355      360      365
149 Arg Ser Phe Arg Ile Thr Ile Leu Pro Gln Leu Tyr Ile Gln Pro Met
150      370      375      380
152 Met Gly Ala Gly Leu Asn Tyr Glu Cys Tyr Arg Phe Gly Ile Ser Pro
153 385      390      395      400
155 Ser Thr Asn Ala Leu Val Ile Gly Ala Thr Val Met Glu Gly Phe Tyr
156      405      410      415
158 Val Ile Phe Asp Arg Ala Gln Lys Arg Val Gly Phe Ala Ala Ser Pro
159      420      425      430
161 Cys Ala Glu Ile Ala Gly Ala Ala Val Ser Glu Ile Ser Gly Pro Phe
162      435      440      445
164 Ser Thr Glu Asp Val Ala Ser Asn Cys Val Pro Ala Gln Ser Leu Ser
165      450      455      460
168 Glu Pro Ile Leu Trp Ile Val Ser Tyr Ala Leu Met Ser Val Cys Gly
169 465      470      475      480
171 Ala Ile Leu Leu Val Leu Ile Val Leu Leu Leu Leu Pro Phe Arg Cys
172      485      490      495
174 Gln Arg Arg Pro Arg Asp Pro Glu Val Val Asn Asp Glu Ser Ser Leu
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177 Val Arg His Arg Trp Lys
178      515

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181 <210> SEQ ID NO: 3

182 <211> LENGTH: 2070

183 <212> TYPE: DNA

184 <213> ORGANISM: Homo sapiens

186 <400> SEQUENCE: 3

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189 ctgcggtctg cccgggagac cgacgaagag cccgaggagc ccggccggag ggcagcttt 180
190 gtggagatgg tggacaacct gaggggcaag tcggggcagg gctactacgt ggagatgacc 240
191 gtgggcagcc ccccgagac gctcaacatc ctggtggata caggcagcag taactttgca 300
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193 taccgggacc tccggaaggg tgtgtatgtg ccctacaccc agggcaagtg ggaaggggag 420
194 ctgggcaccc acctggtaag catcccccat ggcccacacg tcaactgtgc tgccaacatt 480
195 gctgccatca ctgaatcaga caagttcttc atcaacggct ccaactggga aggcattctg 540
196 gggctggcct atgctgagat tgccaggcct gacgactccc tggagccttt ctttgactct 600
197 ctggttaaagc agaccacagt tcccaacctc ttctccctgc acctttgtgg tgctggcttc 660
198 cccctcaacc agtctgaagt gctggcctct gtcggaggga gcatgatcat tggaggtatc 720
199 gaccactcgc tgtacacagg cagtctctgg tatacaccca tccggcgagg gtggtattat 780
200 gaggtcatca ttgtgcgggt ggagatcaat ggacaggatc tgaaaatgga ctgcaaggag 840
201 tacaactatg acaagagcat tgtggacagt ggcaccacca accttcgttt gcccaagaaa 900

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204 ttcccagtc tctcactcta cctaattgggt gaggttacca accagtcctt ccgcatcacc 1080
205 atccttccgc agcaatacct gcggccagtg gaagatgttg ccacgtccca agacgactgt 1140
206 tacaagtttg ccatctcaca gtcattccag ggcactgtta tgggagctgt tatcatggag 1200
207 ggcttctacg ttgtctttga tcgggcccga aaacgaattg gctttgctgt cagcgcttgc 1260
208 catgtgcacg atgagttcag gacggcagcg gtggaaggcc cttttgtcac cttggacatg 1320
209 gaagactgtg gctacaacat tccacagaca gatgagtcaa cctcatgac catagcctat 1380
210 gtcattggctg ccatctgcgc cctcttcatt ctgccactct gcctcatggt gtgtcagtgg 1440
211 cgctgcctcc gctgcctgcg ccagcagcat gatgactttg ctgatgacat ctccctgctg 1500
212 aagtgaggag gcccatgggc agaagataga gattcccctg gaccacacct ccgtggttca 1560
213 ctttggtcac aagtaggaga cacagatggc acctgtggcc agagcacctc aggaccctcc 1620
214 ccaccacca aatgcctctg ccttgatgga gaagggaaaag gctggcaagg tgggttccag 1680
215 ggactgtacc tgtaggaaac agaaaagaga agaaagaagc actctgctgg cggaataact 1740
216 cttggtcacc tcaaatttaa gtccggaaat tctgctgctt gaaacttcag ccctgaacct 1800
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218 gtactggcat cacacgcagg ttaccttggc gtgtgtccct gtggtaccct ggcagagaag 1920
219 agaccaagct tgtttccctg ctggccaaag tcagtaggag aggatgcaca gtttgctatt 1980
220 tgcttttagag acagggactg tataaacaag cctaacattg gtgcaaagat tgcctcttga 2040
221 attaaaaaaaa aaaaaaaaaa aaaaaaaaaa
222                                     2070

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223 <210> SEQ ID NO: 4

224 <211> LENGTH: 501

225 <212> TYPE: PRT

226 <213> ORGANISM: Homo sapiens

228 <400> SEQUENCE: 4

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233           20           25           30
235 Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
236           35           40           45
238 Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
239           50           55           60
241 Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
242   65           70           75           80
244 Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
245           85           90           95
247 Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
248           100          105          110
251 Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
252           115          120          125
255 Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
256           130          135          140
258 Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
259   145          150          155          160
261 Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
262           165          170          175
264 Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
265           180          185          190

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267 Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro
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270 Asn Leu Phe Ser Leu His Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln
271      210      215      220
273 Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
274 225      230      235      240
276 Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
277      245      250      255
279 Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
280      260      265      270
282 Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val
283      275      280      285
285 Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala
286      290      295      300
288 Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp
289 305      310      315      320
291 Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
292      325      330      335
294 Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
295      340      345      350
297 Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
298      355      360      365
300 Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
301      370      375      380
303 Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu
304 385      390      395      400
306 Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala
307      405      410      415
309 Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu
310      420      425      430
313 Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro
314      435      440      445
316 Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala
317      450      455      460
319 Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp
320 465      470      475      480
322 Arg Cys Leu Arg Cys Leu Arg Gln Gln His Asp Asp Phe Ala Asp Asp
323      485      490      495
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330 <211> LENGTH: 1977
331 <212> TYPE: DNA
332 <213> ORGANISM: Homo sapiens
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337 ctgcggctgc cccgggagac cgacgaagag cccgaggagc ccggccggag ggcagcttt 180
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L:12 M:270 C: Current Application Number differs, Replaced Application Number

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date